Name: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Date: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Period: \_\_\_\_\_\_\_

**Hardy Weinberg Equilibrium Math Tutorial**

Mrs. Krouse, AP Biology, 2015-2016

**Background Information:** Recall from our Unit 1, Part 4 Notes (Hardy Weinberg Equilibrium) that populations in Hardy Weinberg Equilibrium are not undergoing evolution. This means that allele and genotype frequencies are not changing over generations. Therefore, the following equations can be used to predict allele and genotype frequencies in any generation for a population in Hardy Weinberg Equilibrium.

|  |  |  |
| --- | --- | --- |
| **Allele Frequencies** | p + q = 1 | p = frequency of the dominant allele (A)  q = frequency of the recessive allele (a) |
| **Genotype Frequencies** | p2 + 2pq + q2 = 1 | p2 = frequency of the homozygous dominant genotype (AA)  2pq = frequency of the heterozygous genotype (Aa)  q2 = frequency of the homozygous recessive genotype (aa) |

Let’s say we were sampling the following population of humans for the trait of height, where “A” represents the dominant tall allele and “a” represents the recessive short allele.

**Population Table:**

|  |  |  |  |
| --- | --- | --- | --- |
| **Individual #** | **Alleles** | **Genotype** | **Phenotype** |
| 1 | “A” and “A” | AA | Tall |
| 2 | “A” and “a” | Aa | Tall |
| 3 | “A” and “a” | Aa | Tall |
| 4 | “a” and “a” | aa | Short |

Out of the above population of humans, we have the following allele frequencies. If this population is in Hardy Weinberg Equilibrium, we expect that these frequencies will stay the same from generation to generation.

**Allele Frequencies:**

|  |  |  |  |
| --- | --- | --- | --- |
| **Allele** | **Calculation Used to Find the Allele Frequency from the Population Above** | **Allele Frequency** | **Term from the Hardy Weinberg Equations Used to Represent this Allele Frequency** |
| A | 4/8 = | 0.5 | p |
| a | 4/8 = | 0.5 | q |

Out of the above population of humans, we have the following genotype frequencies. If this population is in Hardy Weinberg Equilibrium, we expect that these frequencies will stay the same from generation to generation.

**Genotype Frequencies:**

|  |  |  |  |
| --- | --- | --- | --- |
| **Genotype** | **Calculation Used to Find the Genotype Frequency from the Population Above** | **Genotype Frequency** | **Term from the Hardy Weinberg Equations Used to Represent this Genotype Frequency** |
| AA | 1/4 = | 0.25 | p2 |
| Aa | 2/4 = | 0.5 | 2pq |
| aa | 1/4 = | 0.25 | q2 |

Out of the population of humans on the previous page, we have the following phenotype frequencies. If this population is in Hardy Weinberg Equilibrium, we expect that these frequencies will stay the same from generation to generation.

**Phenotype Frequencies:**

|  |  |  |  |
| --- | --- | --- | --- |
| **Phenotype** | **Calculation Used to Find the Phenotype Frequency from the Population Above** | **Phenotype Frequency** | **Term from the Hardy Weinberg Equations Used to Represent this Phenotype Frequency** |
| Tall | 3/4 = | 0.75 | p2 + 2pq |
| Short | 1/4 = | 0.25 | q2 |

“p2 + 2pq” is used to represent the frequency of the dominant phenotype because there are two genotypes, “AA” (frequency represented by p2) and “Aa” (frequency represented by 2pq), that can result in the dominant phenotype (i.e. tall). “q2” is used to represent the frequency of the recessive phenotype because there is only one genotype, “aa” (frequency represented by q2), that can result in the recessive phenotype (i.e. short).

Let’s say we are only told the allele frequencies (p = 0.5 and q = 0.5) for the population of humans on the previous page. We could use these frequencies alone to determine the genotype and phenotype frequencies for the population, so long as it is in Hardy Weinberg Equilibrium. Note that these genotype and phenotype frequencies match up exactly with those we calculated by sampling the population.

**Calculating Genotype and Phenotype Frequencies:**

|  |  |  |  |
| --- | --- | --- | --- |
| **Frequency to be Determined** | **Term from the Hardy Weinberg Equations Used to Represent this Frequency** | **Calculation Used to Find this Frequency from the Given Allele Frequencies** | **Calculated Frequency** |
| Frequency of the homozygous dominant genotype (AA) | p2 | p = 0.5 🡪 p2 = (0.5)2 = | 0.25 |
| Frequency of the heterozygous genotype (Aa) | 2pq | p = 0.5, q = 0.5 🡪 2pq = (2 x 0.5 x 0.5) = | 0.50 |
| Frequency of the homozygous recessive genotype (aa) | q2 | q = 0.5 🡪 q2 = (0.5)2 = | 0.25 |
| Frequency of the dominant phenotype (Tall) | p2 + 2pq | p = 0.5, q = 0.5 🡪 p2 + 2pq = [(0.5)2 + (2 x 0.5 x 0.5)] = | 0.75 |
| Frequency of the recessive phenotype (Short) | q2 | q = 0.5 🡪 q2 = (0.5)2 = | 0.25 |

If we are given the number of individuals for the population of humans on the previous page (4 people), we can use the genotype and phenotype decimal frequencies calculated in the chart above to determine the actual whole number of people in the population with each genotype and phenotype.

|  |  |  |  |
| --- | --- | --- | --- |
| **Genotype or Phenotype** | **Calculated Frequency** | **Calculation to Determine Whole Number of People with this Genotype or Phenotype** | **Whole Number of People with this Genotype or Phenotype** |
| Homozygous dominant genotype (AA) | 0.25 | 0.25 x 4 = | 1 |
| Heterozygous genotype (Aa) | 0.50 | 0.50 x 4 = | 2 |
| Homozygous recessive genotype (aa) | 0.25 | 0.25 x 4 = | 1 |
| Frequency of the dominant phenotype (Tall) | 0.75 | 0.75 x 4 = | 3 |
| Frequency of the recessive phenotype (Short) | 0.25 | 0.25 x 4 | 1 |

When solving Hardy Weinberg math problems, you should follow the procedure outlined below…

1. Identify which “terms” from the Hardy Weinberg equations you are GIVEN
2. Identify which “terms” from the Hardy Weinberg equations you are asked to FIND
3. Show your CALCULATIONS to go from what you are given to what you are asked to find

I will use this procedure to show you how to solve the four sample problems below. (The final answer for each sample problem is bolded.) Then, you will move on to the Hardy Weinberg Practice Worksheet.

**Sample Problem #1:**

The frequency of two alleles in a gene pool is 0.1 (A) and 0.9 (a). What is the percentage in the population of the heterozygous individuals?

1. Given: p = 0.1 and q = 0.9
2. Find: 2pq x 100 (because 2pq is a decimal frequency and we need a percentage)
3. Calculations: [(2 x 0.1 x 0.9) x 100] = **18%**

**Sample Problem #2:**

Allele (B), for white wool, is dominant over allele (b), for black wool. In a sample of 900 sheep, 891 are white and 9 are black. How many sheep are homozygous dominant for coat color?

1. Given: q2 = 9/900 = 0.01
2. Find: p2 x 900 (because p2 is a decimal frequency and we need a whole number of sheep out of the population of 900)
3. Calculations:

= q = = 0.1

p + q = 1 🡪 p = 1-q 🡪 p = 1-0.1 = 0.9

p2 = (0.9)2 = 0.81

p2 x 900 = 0.81 x 900 = **729 sheep**

**Sample Problem #3:**

The allele (T), the ability to taste a particular chemical, is dominant to allele (t), the inability to taste it. At Cornell University, out of 400 surveyed students, 64 were found to be non-tasters. What is the frequency of the recessive allele?

1. Given: q2 = 64/400 = 0.16
2. Find: q
3. Calculations: = q = = **0.4**

**Sample Problem #4**

In humans, Rh positive blood is produced by the dominant gene (R), while Rh negative blood is produced by the allele (r). If the frequency of “r” is 0.4, what percentage of the population has Rh positive blood (the dominant phenotype)?

1. Given: q = 0.4
2. Find: (p2 + 2pq) x 100 (because “p2 + 2pq” is a decimal frequency and we need a percentage)
3. Calculations:

p + q = 1 🡪 p = 1-q 🡪 p = 1-0.4 = 0.6

p2 = (0.6)2 = 0.36

2pq = (2 x 0.6 x 0.4) = 0.48

(p2 + 2pq) x 100 = (0.36 + 0.48) x 100 = 0.84 x 100 = **84%**